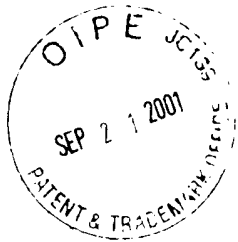


SEQUENCE LISTING

(1) GENERAL INFORMATION:



- (i) APPLICANT: DECKER, Heinrich
- (ii) TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUDESCENS GLA.O AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: FOLEY & LARDNER
  - (B) STREET: 3000 K Street, N.W.
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/194,905
  - (B) FILING DATE: 19-JUL-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/EP97/02826
  - (B) FILING DATE: 30-MAY-1997
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: DE 19622783.6
  - (B) FILING DATE: 07-JUN-1996
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Granados, Patricia D.
  - (B) REGISTRATION NUMBER: 33,683
  - (C) REFERENCE/DOCKET NUMBER: 026083/0193
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202) 672-5300
  - (B) TELEFAX: (202) 672-5399

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CSGGSGSSGC SGGSTTCATS GG

22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGWVCTGGY VSGGSCCGTA GTTG

24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|  |     |
|--|-----|
| CCCGGGGGGGG GCGGGGGTTCA TCGGCTCCGC CTACGTCCGC CGGCTCCTGT CGCCCGGGGGC | 60  |
| CCCCGGCGGGC GTCGCGGTGA CCGTCTCGA CAAACTCACC TACGCGGGCA GCTCGCCCG     | 120 |
| CCTGCACGCG GTGCGTGACC ATCCCGGCT CACCTCGTC CAGGGCGACG TGTGGACAC       | 180 |
| CGCGCTCGTC GACACGCTGG CCGCGGGCA CGACGATC GTGCACTCG CGGCGAGTC         | 240 |
| GCACTCGAC CGCTCCATCA CCGACGCGG TGCTTCACC CGCACCAACG TGCTGGGAC        | 300 |
| CCAGGTCTTG CTGACGCGG CGCTCGGCA CGGTGTGCG ACCCTCGTGC ACGTCTCCAC       | 360 |
| CGACGAGGTG TACGGCTCCC TCCCGCACGG GGCGCGCGG GASAGCGACC CCTGCTCCC      | 420 |
| GACCTCGCG TACGGGGGT GGAAGGGGG CTGGGACCTC ATGGCGCTCG CCGACACCG        | 480 |
| CACCCACGGC CTGGACGTCC GGGTGACCG CTGTTGGAAC AACTACGGCC CGCACAGTT      | 540 |
| CCCGGG   | 546 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CCCCGGGTGC TGGTAGGGGC CGTAGTTGTT GGAGCAGCGG GTGATGCGCA CGTCCAGGCC      60
GTGGCTGACG TGCATGGCCA GCGCGAGCAG GTCGCCCCGAC GCCTTGGAGG TGGCATAGGG      120
GCTGTTGGGG CGCAGCGGCT CGTCCTCCGT CCACGACCCC GTCTCCAGCG AGCCGTAGAC      180
CTCGTCGGTG GACACCTGCA CGAAGGGGGC CACGCCGTGC CGCAGGGCCG CGTCGAGGAG      240
TGTCTGCGTG CCGCCGGCGT TGGTCCGCAC GAACGCGGCG GCATCGAGCA GCGAGCGGTC      300
CACGTGCGAC TGGGCGGCGA GGTGCACGAC CTGCTCTTGG CCGGGCATGA CCGGTCGAC      360
CAGGTCCGCG TCGCAGATGT CGCCGTGGAC GAAGCGCAGC CCGGGGTGGT CCGCGACCGG      420
GTCGAGGTTG GCGAGGTTGC CGGCGTAGCT CAGGGCGTCG AGCACGGTGA CGACGGCGTC      480
GGGCGGCCCG TCCGGACCGA GGAGGGTGCG GACGTAGTGC GAGCCCATGA ACCCGGCCGC      540
C
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Ala Ala Gly Phe Met Gly Ser His Tyr Val Arg Thr Leu Leu Gly Pro
1           5           10           15
Asp Gly Pro Pro Asp Ala Val Val Thr Val Leu Asp Ala Leu Ser Tyr
20           25           30
Ala Gly Asn Leu Ala Asn Leu Asp Pro Val Arg Asp His Pro Arg Leu
35           40           45
Arg Phe Val His Gly Asp Ile Cys Asp Ala Asp Leu Val Asp Arg Val
50           55           60
Met Ala Gly Gln Asp Gln Val Val His Leu Ala Ala Glu Ser His Val
65           70           75           80
Asp Arg Ser Leu Leu Asp Ala Ala Ala Phe Val Arg Thr Asn Ala Gly
85           90           95
Gly Thr Gln Thr Leu Leu Asp Ala Ala Leu Arg His Gly Val Ala Pro
100          105          110
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Val | Gln | Val | Ser | Thr | Asp | Glu | Val | Tyr | Gly | Ser | Leu | Glu | Thr | Gly |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Trp | Thr | Glu | Asp | Glu | Pro | Leu | Arg | Pro | Asn | Ser | Pro | Tyr | Ala | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Lys | Ala | Ser | Gly | Asp | Leu | Leu | Ala | Leu | Ala | Met | His | Val | Ser | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Leu | Asp | Val | Arg | Ile | Thr | Arg | Cys | Ser | Asn | Asn | Tyr | Gly | Pro | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | His | Pro | Gly |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Gly | Ala | Gly | Phe | Ile | Gly | Ser | Ala | Tyr | Val | Arg | Arg | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Pro | Gly | Ala | Pro | Gly | Gly | Val | Ala | Val | Thr | Val | Leu | Asp | Lys | Leu |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Thr | Tyr | Ala | Gly | Ser | Leu | Ala | Arg | Leu | His | Ala | Val | Arg | Asp | His | Pro |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Thr | Phe | Val | Gln | Gly | Asp | Val | Cys | Asp | Thr | Ala | Leu | Val | Asp |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Leu | Ala | Ala | Arg | His | Asp | Asp | Ile | Val | His | Phe | Ala | Ala | Glu | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Val | Asp | Arg | Ser | Ile | Thr | Asp | Ser | Gly | Ala | Phe | Thr | Arg | Thr | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Gly | Thr | Gln | Val | Leu | Leu | Asp | Ala | Ala | Leu | Arg | His | Gly | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Arg | Thr | Leu | Val | His | Val | Ser | Thr | Asp | Glu | Val | Tyr | Gly | Ser | Leu | Pro |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Gly | Ala | Ala | Ala | Glu | Ser | Asp | Pro | Leu | Leu | Pro | Thr | Ser | Pro | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Ser | Lys | Ala | Ala | Ser | Asp | Leu | Met | Ala | Leu | Ala | His | His | Arg |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Thr | His | Gly | Leu | Asp | Val | Arg | Val | Thr | Arg | Cys | Ser | Asn | Asn | Tyr | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | His | Gln | Phe | Pro |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|   |      |
|---|------|
| CTGCAGGGTT CCTGGTGCA CGACCCGCC CTGGTCGACG ACCAGGGCGC TGTGCGAGAT   | 60   |
| CGCGGGGATG TGGGCGATGT GCTGGCTGCT GAGCAGCAGC CTGCTGCCCA GTTCCGGTG  | 120  |
| GGGCGGGTTG ACCAGCCGGC GCACCGCGTC CTTCAGCACC ATGTGAGGGC CGATCGTGGG | 180  |
| CTCGTCCCAg AACAGCACGG CCGGGTCTG CAGCAGGCTC GCCGCGATCT CGGCGCGCAT  | 240  |
| GGGCTGTCCG AGGCTGAGCT GCCGCACGGG GGTGGACCCC AGCGCGTCGA TGTGAGGAG  | 300  |
| GTCCCGGAAC AAGGCGAGGT TGGGCGGTA GACCGGTCCG GGGATGTCGT AGATGCGGCG  | 360  |
| CAGSATGCGG AAGGAGTCGG GTACGACAG GTCCACCAAG AGCTGGCTGC GCTGGCCGAA  | 420  |
| GACGACGCG ATCTGTGCGG CGTTGCGCTG CCGGTGCCGG TAGGGCTCCA GCCCGGCGAC  | 480  |
| CGTGCAGCGG CCGGAGGTGG GGGTCATGAT GCGGTCAGC ATCTTGATCG TGGTCGACTT  | 540  |
| GCCGGCTCCG TTGGCGCCGA TGTAGGCGGT CTTCGTGCGG GCGGTATCT CGAAGGAGAC  | 600  |
| GTGTCGACG GGGCGCAGGA CGGGTACCG GGGGTCAGG AGGGTGGAGA GGTGCCGAG     | 660  |
| CAGGCCGGGC TGCGTTCCG CCAGCCGGAA CTCCTTGACG AGGTGTTCCG CCACGATCAC  | 720  |
| GCGATCACCC GTTCGACGGC CGTCTCCAGC AGGCGCAGGC CCTCGTCGAG CAGCGCCTCG | 780  |
| TGGAGGGTGA ACGGCGGTGC CAGCCGCAGG ATGTGGCCGC CCAGGGAGGT GCGCAGCCCC | 840  |
| AGGTGAGGG CGGTGGTGTA GACGGCCCGG GCGGTCTCGG GGGCGGGTGC CCGGCCGACG  | 900  |
| GCGTCGGTGA CGAACTCCAG GCGCCACAGC AGTCCGAGGC CGGTACCTG GCGAGCTGG   | 960  |
| GGGAAGCGGG ACTCCAGGGC GCGCAGCCGC TCCTGGATGA GTCGCGGAG GACGCGCAGG  | 1020 |
| CGGTGATCA GCGGTCGGG CTGACGACC TCCAGCGTGG CGCGGGGGGC GGGATCCCC     | 1080 |
| AGTGGGTTGC TGCGTACGT CGAGGCGTAC GCGCCGGGGT GGCGGCTCC GGCCTGCGCA   | 1140 |
| GCTTCCGCGC GTGGGGCCAG CAGGGCGAAG GGAATCCGC TCGCGGTGCC CTTGGACAGC  | 1200 |
| ATGCCCAGGT CCGGCTCGAT GCGAACAAT TGGCTGGCGA GGAAGGCGCC GGTGCGCCCG  | 1260 |
| CGCGCGGTGA GAACTCGTC GCGGACGAGC AGCAGCGCGC CGTCCCGGCA GCGGCGGGG   | 1320 |
| ATCCGCTCC AGTAGCGGG GGGCGGCAAG ATGACGCTG CCGCGCGGAG GACGGGTTCC    | 1380 |
| AAGACCAGGG CCGAGACGTT GGGCTTCTCC GCGATGTGCC GCGGCACGAG GGTGCGCAC  | 1440 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| CGCACGTGCG | ACGAGGGGTA | CTCCAGGCC  | AGGGGACAGC | GGTAGCCAGT | AGGGGCTGTA | 1500 |
| GCCAGCACGC | TGTTGCCGCT | GAAGGCCTGG | TGGCCGATGT | CCCAGTGGAC | CAGCATCCGG | 1560 |
| GCGCCCATGG | TCTTGCCGTG | GAAGCCGTGG | CGCAGGGCGC | AGATCCGGTT | GCGGCCCGGC | 1620 |
| GCGCGGGTCG | CCTGGACGAC | CCGCAGGGCG | GCCTCGACCA | CCTCCGCGCC | GGTGGAGAA  | 1680 |
| AAGGCGTAGG | TGTCGAGCTG | TTGGGGCAGC | AGCCTGGCGA | GCAGTTCCAG | CAGGCCGGCG | 1740 |
| CGGTCCGGCG | TGGCGCTGTC | GTGGACGTTG | CACAGGCGGC | GGGCCTGGGT | GGTGAGTGCC | 1800 |
| TCGACGACCT | CCGGGTGCC  | GTGGCCCACT | GACTGGGTGA | GGGTCCCGGC | CGCGAAGTCG | 1860 |
| AGGTACTGGT | TGCCGTCCAG | GTGGGTGAGA | ACGGGACCGC | GTCCCTCGGC | GAAGAACCAG | 1920 |
| CGTCCGTGGA | CGGCTTCCTC | GGAGGCGGCC | GGCGCCAGGT | GGCGGGGCTC | CCGTGCCAGG | 1980 |
| TGTTGTGTCT | GGGTAAAGCC | TGTCATCGCT | GGCTGTGCTC | GTGGGACCGG | CTGACGGGAT | 2040 |
| CGCCGGCGAA | CTGCGTTGTC | GCGCACCACG | GTTGGGGCGG | CTCGGCGCTG | AGTCAAAAC  | 2100 |
| TTGAACACAC | ACCGCTGCAA | GAGTTTGCGG | GTTGTTTCAG | AAAGTTGTTG | CGAGCGGGCC | 2160 |
| CGGCACTCTG | GTTGAGTCGA | CGTGCTTACG | GCGCCACCA  | GGCTCACGTT | CGAGGAGGGA | 2220 |
| CCTGTGAGAA | CAAGCCCGCA | GACCGACCGG | CTCCCGCGGA | GGCCGAGGTG | AAGGCCTGCG | 2280 |
| TCCTGGCAGG | TGGAACCGGC | AGCAGACTGA | GGCGGTTTAC | CCACACCGCC | GCCAAGCAGC | 2340 |
| TGCTCCCAT  | CGCCAACAA  | CCCGTGCTCT | TCTACGGGCT | GGAGTCCCTC | GCGCGGGCGG | 2400 |
| GTGTCCGGGA | GGCCGGGCTC | GTGTGGGCG  | GCTACGGCGG | GGAGATCCGC | GAAGTCACCG | 2460 |
| GCGACGGCAC | CGCGTTCCGG | TTACGCATCA | CCTACCTCCA | CCAGCCCCGC | CCGTCTGGTC | 2520 |
| TGGGCGACGC | GSTGGCGATC | GCCCCGGGCT | TCCTGGGGGA | CGACGACTTC | CTGTGTGACC | 2580 |
| TGGGGGACAA | CTACCTGCC  | CAGGCGGTCA | CCGACTTGCG | CCGCCAATCG | GCCGCGGATC | 2640 |
| CGCGGGCGGC | CCGGCTGCTG | CTCACCCCGG | TGGGGGACCC | GTCCGCTTC  | GGGTGCGCGG | 2700 |
| AGGTGACGC  | GGACGGGAAC | GTGCTGGGCT | TGGAGGAGAA | ACCCGACGTC | CGCGCGAGCT | 2760 |
| CGCTCGGCT  | CATCGGCGTG | TACGCCTTCA | GCCCCGGCGT | CCACGAGGCG | GTACGGGCCA | 2820 |
| TCACCCCTC  | CGCCCGCGGC | GAGCTGGAGA | TCACCCACGC | CGTGCACTGG | ATGATCGAC  | 2880 |
| GGGGCTGCG  | CGTACGGGCC | GAGACCACCA | CCCGGCCCTG | GGGGACACCC | GGCAGCGCGG | 2940 |
| AGGACATGCT | GGAGGTCAAC | CGTCACGTCC | TGGACGGACT | GGAGGGCCGC | ATCGAGGGGA | 3000 |
| AGGTGACGC  | GCACAGCACG | CTGGTCGGCC | GSTCCGGST  | GGCCGAAGGC | GCGATCGTGC | 3060 |
| GGGGGTGACA | CGTGGTGGGC | CCGGTGGTGA | TGGGCGCGGG | TGCCGTGCTC | AGCAACTGCA | 3120 |
| GTGTGGGCC  | GTACACCTCC | ATCGGGGAGG | AATGCCGGST | CGAGGACAGC | GCCATCGAST | 3180 |
| ACTCGGTCT  | GCTGGCGGGC | GCCCAGGTGG | AGGGGGGCTC | CCGATCGAG  | GGGTGCTTCA | 3240 |
| TGGGCGGGG  | CGCGGTGCTC | GGCCCGGGCC | CCGTGTCTCC | GCAGGCTTAC | CGACTGCTGA | 3300 |
| TGGGCGACCA | CAGCAAGGTG | TATCTCACCC | CATGACCACG | ACCATGCTCG | TCACCGGGGG | 3360 |

|   |      |
|---|------|
| AGCGGGCTTC ATTCGCTCCG CCTACGTCCG CCGGCTCCTG TCGCCCGGGG CCCCCGGGG  | 3420 |
| CGTCGCGGTG ACGTCCCTCG ACAAACCTAC CTACGCGGGG AGCTCGGCC GCTGCAACGC  | 3480 |
| GCTGCGTGAA CATCCCGGGC TCACCTTCGT CCAGGGGAGC GTGTGCGACA CCGCGCTCGT | 3540 |
| CGACACGCTG GCGCGCGGGC ACGACGACAT CGTGCACTTC GCGGCGAGT CGCACGTGGA  | 3600 |
| CCGCTCCATC ACGACAGCG GTGCCTTCAC CCGCACCAAC GTGCTGGGCA CCCAGGTCT   | 3660 |
| GCTCGACGGC GCGCTCCGGC AGGTGTGGC CACCTTCGTG CAGTCTCCA CGACGAGGT    | 3720 |
| GTACGGCTCC CTCGCCACG GGGCGCGGC GGAGAGCGAC CCGTCTTC CGACCTCGGC     | 3780 |
| GTACGCGGGC TCGAAGGGG CCTCGGACT CATGGGCTC GCGCACACC GCACCCAGG      | 3840 |
| CCTGGACGTC CCGGTGACCC GGTGTTCGAA CAACTTGGG CCCCACCAGC ATCCCGAGAA  | 3900 |
| GCTCATACCG CGCTTCCTGA CCAGCTCTCT GTCCGGGGG ACCGTTCGCC TCTACGGCGA  | 3960 |
| CGGGCGGCAC GTGCGGACT GGCTGCAGT CGACGACAC GTACGGGCGG TCGAACTCGT    | 4020 |
| CCGCGTGTG GCGCGCGGG GAGAGATCTA CAACATCGG GCGGGACCT CGCTGCCCAA     | 4080 |
| CCTGGAGCTC ACGCACGGT TGCTCGACT GTGCGGGG GCGCGGAGC GCATCTCCA       | 4140 |
| CGTCGAGAAC CGCAAGGGG ACGACCGGG CTACGGGTC GACACAGCA AGATCACCGC     | 4200 |
| GGAACCTCGT TACCGGCCG GACCGACTT CCGGACCGG CTGGCGACA CCGCGAAGTG     | 4260 |
| GTACGAGCGG CACGAGGACT GGTGGCGTC CCTGCTGCC GCGACATGAC GTGGGGCGG    | 4320 |
| ACCGCAACCA CCGGCCCCG CCGGCACAC GCGCGCGG GCGGTGGC GCGCGGTGAG       | 4380 |
| CGTCCGTGAG CCGGGCGCG GCGCCCCG GCGCGGGG CCGTGGACC CCGGACGAC        | 4440 |
| AGTTCGGCA TGAAGACGAA TTCGGTGGG GCGGGGGG TTGCGTCAT CTCTCCAGC       | 4500 |
| AGTGGCTCA CCGCGACCTG CCGATGCG TTGAGGGT GTTGATGT GTTAGGGGA         | 4560 |
| GGTCCGTGA AGGCAATGAG CCGCGAGTG TCGAAGCGA CCAGGAGAT GTTACCGGA      | 4620 |
| ACCGTGAGAC CCGGCGGGG CCGGGCGCG ACGGGGCGA GCGCATCAT GTGCTGGG       | 4680 |
| CACATGACCG CGGTGACGC CAGGTGATC AGCGGGAG CCGGGGCTG GCGCGCTCC       | 4740 |
| AGGAGAGACA GCGAGTGTG CACGAGTTC TCGGATCCC GCGCGACAC TCCAGGTGC      | 4800 |
| TCCCGCAGG CCGGCGGAA CCGCTGATC TTGCTGCA CCGGCACGA GCGGGGGGG        | 4860 |
| CGACGCGGA GCGGACGG CTGCTGCC AGCTCGCCA GTGCGGAC GCGGAGGCG          | 4920 |
| ATCGCGGCC GTCTCTGGG GGAGAGGAG GTGCTTGA TTGGGGCGA GAACCGTTC        | 4980 |
| ACGAGAGCA AGGGAACCTG CCGCTGCTC AGCGGGCGT ACGTCCGGT CTCGGGGTG      | 5040 |
| GTGTCCGGT GCAGTCGGA GACGAAGAT ATGCGGACA CCGGCGGTC CACGAGCATC      | 5100 |
| TCCGTGAGTT CTTCTCGGT CGAGCGGCC GGGGTCTGG TGGGAGCAC GGGGTGTAG      | 5160 |
| CCCTGACGG TGAGGGCTG CCGATCAC TGGGAGTG GCGGGAAGAA GGGGTGTCT        | 5220 |
| AGTTGGGGG TGACAGTCC GACGAGTCT GCGGGGGT GTGGGGGG GTGCTGTAG         | 5280 |

|   |      |
|---|------|
| CCCAGCGCGT CCAGTGCGGT CAGCACCGAG TCGCGGGTGC CGGTGGCCAC ACCGCGCGCA | 5340 |
| CCGTTACGCA CCGGGCTGAC CGTGGCCTTG CTGACGCCCG CCCGGGCTGC GATGTGGGG  | 5400 |
| AGCCGATGG TCATGGCAAC GCACTCTACC TGTCGGGGCG TCAGGGCGTG CCCACCGCGC  | 5460 |
| GCGGAACCGG CGGACTGGG GGCACGGCCC GTCCGCCGCC CACGGACCA CCGCCCGAAA   | 5520 |
| CGATGGCTGA AAATGCTTGC AGCAAATTGC CGCAACGTCT TTCGGCGGCT TTTCGATCCT | 5580 |
| GTTAGTTTC TGGCAACCCC GCGGCCGCGC AGAAGCGGTT GGCCTGAGGC GTCCAGACCT  | 5640 |
| CCGCCCGATT CCGGGATCAC TCAGGGGAGT TCACAATGG GCGTGGCATT GCGGCCACCG  | 5700 |
| CGCTGTTCCG GGTGTGGCC ATGACGGCAT CGGCGTGTGG CGGGGGCGAC AACGGCGGAA  | 5760 |
| GCGGTACCGA CGGGGGCGGC ACGGAGCTGT CCGGGACCGT CACCTTCTGG GACACGTCCA | 5820 |
| ACGAAGCGCA GAAGGGGAGG TACCAGGCC TCGGGGAGGG CTTCGAGAAG GAGCACCGCA  | 5880 |
| AGGTGGACGT CAAGTACGTC AACGTCCCGT TCGGGGAGGC GAACGCCAAG TTCAAGAACG | 5940 |
| CCGCGGGGG CAATCCGCT GCGCCGAGG TGATGGTAC GGAGGTGGCC TGGGTGGGG      | 6000 |
| ACTTGGCCAG CATCGGCTAC CTGCCCCCGC TCGACGGCAC GCGCGCCCTC GACGACGGGT | 6060 |
| CGGACCACT TCCCGAGGC GGCAGACCA GGTACGAGGG GAAGACCTAC GCGGTCCCGC    | 6120 |
| AGGTGATCGA GAGCTGGGG CTCTTCTACA ACAAGGAACT GCTGAGGAAG GCGGTGTGG   | 6180 |
| AGGTGCCGGG CTCCTCGCC GAGCTGAAGA CGGCCGCCGC CGAGATCACC GAGAAGACCG  | 6240 |
| GCGCGAGCGG CCTCTACTGC GGGCGACGA CCGTACTTG GTTCTGCCC TACCTCTACG    | 6300 |
| GGGAGGGGG CGACTGGTC GACGAGAAAG ACAAGACCGT CACGGTCGAC GACGAAGCGG   | 6360 |
| GTGTGGCGC CTACCGGTC ATCAAGGACC TCGTGGACAG CAAGGCGGCC ATCACCGAGG   | 6420 |
| CGTCGAGGG CTGGAAACA ATGCAGAAC CCTTCAAGTC GGGCAAGGTC GCCATGATGG    | 6480 |
| TCAACGGCCC CTGGGCCATC GAGGACGTCA AGGCGGGAGC CCGCTTCAAG GACGCGGGCA | 6540 |
| ACCTGGGGGT CGGCCCGCT CCGGCCGGCA GTGCCGGACA GGGCTCTCCC CAGGGCGGGT  | 6600 |
| GGAACCTCTC GGTGTACGG GGCTCGAAGA ACCTCGACGC CTCCTACGCC TTCGTGAAGT  | 6660 |
| ACATGAGCTC CGCAAGGTG CAGCAGCAGA CCACCGAGAA GCTGAGCCTG CTGCCACCC   | 6720 |
| GCACGTCCGT CTACGAGGTC CCGTCGCTG CGGACAACGA GATGGTGAAG TTCTTCAAGT  | 6780 |
| CGGCCGTGCA CAAGGCCCTC GAACGGCCGT GGATCGCCGA GGGCAATGCC CTCTTCGAGC | 6840 |
| CGATCGGGCT GCAG   | 6854 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STANDARDS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Ile Val Ala Glu His Leu Val Lys Glu Phe Arg Leu Ala Glu Arg  
1 5 10 15  
Glu Pro Gly Leu Leu Gly Ser Leu Ser Thr Leu Leu Thr Arg Arg Tyr  
20 25 30  
Arg Val Val Arg Ala Val Asp Asp Val Ser Phe Glu Ile Pro Ala Gly  
35 40 45  
Thr Lys Thr Ala Tyr Ile Gly Ala Asn Gly Ala Gly Lys Ser Thr Thr  
50 55 60  
Ile Lys Met Leu Thr Gly Ile Met Thr Pro Thr Ser Gly Arg Cys Thr  
65 70 75 80  
Val Ala Gly Leu Glu Pro Tyr Arg His Arg Gln Arg Asn Ala Arg Thr  
85 90 95  
Ile Gly Val Val Phe Gly Gln Arg Ser Gln Leu Trp Trp Asp Leu Ser  
100 105 110  
Val Pro Asp Ser Phe Arg Ile Leu Arg Arg Ile Tyr Asp Ile Pro Gly  
115 120 125  
Pro Val Tyr Arg Arg Asn Leu Ala Leu Phe Arg Asp Leu Leu Asp Ile  
130 135 140  
Asp Ala Leu Gly Ser Thr Pro Val Arg Gln Leu Ser Leu Gly Gln Arg  
145 150 155 160  
Met Arg Ala Glu Ile Ala Ala Ser Leu Leu His Asp Pro Ala Val Leu  
165 170 175  
Phe Trp Asp Glu Pro Thr Ile Gly Leu Asp Met Val Leu Lys Asp Ala  
180 185 190  
Val Arg Arg Leu Val Asn Arg Ala His Arg Glu Leu Gly Thr Thr Val  
195 200 205  
Val Leu Thr Ser His Asp Ile Ala Asp Ile Ala Ala Ile Cys Asp Ser  
210 215 220  
Ala Leu Val Val Asp Gln Gly Arg Val Val His Gln Gly Thr Leu Gln  
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Gly Leu Arg Gln Thr Gln His Leu Ala Arg Glu Ala Arg His  
1 5 10 15  
Leu Ala Pro Gly Ala Ser Glu Glu Ala Val His Gly Arg Arg Val Phe  
20 25 30  
Ala Glu Gly Arg Gly Pro Val Leu Thr Asp Leu Asp Gly Asn Gln Tyr  
35 40 45  
Leu Asp Phe Ala Ala Gly Thr Leu Thr Gln Ser Leu Gly His Gly His  
50 55 60  
Pro Glu Val Val Glu Ala Leu Thr Thr Gln Ala Arg Arg Leu Trp Asn  
65 70 75 80  
Val His Asp Ser Ala Thr Pro Asp Arg Ala Gly Leu Leu Glu Leu Leu  
85 90 95  
Ala Arg Leu Leu Pro Glu Gln Leu Asp Thr Tyr Ala Phe Phe Ser Thr  
100 105 110  
Gly Ala Glu Val Val Glu Ala Ala Leu Arg Val Val Gln Ala Thr Ala  
115 120 125  
Ala Pro Gly Arg Asn Arg Ile Cys Ala Leu Arg His Gly Phe His Gly  
130 135 140  
Lys Thr Met Gly Ala Arg Met Leu Val His Trp Asp Ile Gly His Gln  
145 150 155 160  
Ala Phe Ser Gly Asn Ser Val Leu Ala Thr Ala Pro Thr Gly Tyr Arg  
165 170 175  
Cys Pro Leu Gly Leu Glu Tyr Pro Ser Cys Asp Val Arg Cys Ala Thr  
180 185 190  
Leu Val Arg Arg His Ile Ala Glu Lys Pro Asn Val Ser Ala Leu Val  
195 200 205  
Phe Glu Pro Val Leu Gly Ala Ala Gly Val Ile Val Pro Pro Pro Gly  
210 215 220  
Tyr Trp Glu Arg Ile Ala Gly Ala Cys Arg Asp Gly Gly Val Leu Leu  
225 230 235 240  
Val Ala Asp Glu Val Leu Thr Gly Gly Gly Arg Thr Gly Ala Phe Leu  
245 250 255  
Ala Ser Glu Leu Phe Gly Ile Glu Pro Asp Leu Ala Met Leu Ser Lys  
260 265 270  
Gly Thr Ala Ser Gly Phe Pro Phe Ala Val Leu Ala Gly Arg Ala Glu  
275 280 285  
Ala Ala Gln Ala Gly Gly Gly His Pro Gly Ala Tyr Ala Ser Thr Tyr  
290 295 300  
Ala Ser Asn Pro Leu Gly Ile Ala Ala Ala Arg Ala Thr Leu Glu Val  
305 310 315 320  
Val Glu Arg Asp Arg Leu Ile Asp Arg Val Arg Val Leu Gly Glu Leu  
325 330 335

Ile Gln Glu Arg Leu Arg Ala Leu Glu Ser Arg Phe Pro Gln Leu Gly  
 340 345 350  
 Gln Val Arg Gly Leu Gly Leu Leu Trp Gly Leu Glu Phe Val Thr Asp  
 355 360 365  
 Ala Val Gly Arg Ala Pro Ala Pro Glu Thr Ala Arg Ala Val Tyr Thr  
 370 375 380  
 Thr Ala Leu Asp Leu Gly Leu Arg Thr Ser Leu Gly Gly His Ile Leu  
 385 390 395 400  
 Arg Leu Ala Pro Pro Phe Thr Leu Asp Glu Ala Leu Leu Asp Glu Gly  
 405 410 415  
 Leu Arg Leu Leu Glu Thr Ala Val Glu Arg Val Ile Ala  
 420 425

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 355 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Lys Ala Leu Val Leu Ala Gly Gly Thr Gly Ser Arg Leu Arg Pro  
 1 5 10 15  
 Phe Thr His Thr Ala Ala Lys Gln Leu Leu Pro Ile Ala Asn Lys Pro  
 20 25 30  
 Val Leu Phe Tyr Ala Leu Glu Ser Leu Ala Ala Ala Gly Val Arg Glu  
 35 40 45  
 Ala Gly Val Val Val Gly Ala Tyr Gly Arg Glu Ile Arg Glu Leu Thr  
 50 55 60  
 Gly Asp Gly Thr Ala Phe Gly Leu Arg Ile Thr Tyr Leu His Gln Pro  
 65 70 75 80  
 Arg Pro Leu Gly Leu Ala His Ala Val Arg Ile Ala Arg Gly Phe Leu  
 85 90 95  
 Gly Asp Asp Asp Phe Leu Leu Tyr Leu Gly Asp Asn Tyr Leu Pro Gln  
 100 105 110  
 Gly Val Thr Asp Phe Ala Arg Gln Ser Ala Ala Asp Pro Ala Ala Ala  
 115 120 125  
 Arg Leu Leu Leu Thr Pro Val Ala Asp Pro Ser Ala Phe Gly Val Ala  
 130 135 140  
 Glu Val Asp Ala Asp Gly Asn Val Leu Arg Leu Glu Glu Lys Pro Asp  
 145 150 155 160

Val Pro Arg Ser Ser Leu Ala Leu Ile Gly Val Tyr Ala Phe Ser Pro  
 165 170 175  
 Ala Val His Glu Ala Val Arg Ala Ile Thr Pro Ser Ala Arg Gly Glu  
 180 185 190  
 Leu Glu Ile Thr His Ala Val Gln Trp Met Ile Asp Arg Gly Leu Arg  
 195 200 205  
 Val Arg Ala Glu Thr Thr Thr Arg Pro Trp Arg Asp Thr Gly Ser Ala  
 210 215 220  
 Glu Asp Met Leu Glu Val Asn Arg His Val Leu Asp Gly Leu Glu Gly  
 225 230 235 240  
 Arg Ile Glu Gly Lys Val Asp Ala His Ser Thr Leu Val Gly Arg Val  
 245 250 255  
 Arg Val Ala Glu Gly Ala Ile Val Arg Gly Ser His Val Val Gly Pro  
 260 265 270  
 Val Val Ile Gly Ala Gly Ala Val Val Ser Asn Ser Ser Val Gly Pro  
 275 280 285  
 Tyr Thr Ser Ile Gly Glu Asp Cys Arg Val Glu Asp Ser Ala Ile Glu  
 290 295 300  
 Tyr Ser Val Leu Leu Arg Gly Ala Gln Val Glu Gly Ala Ser Arg Ile  
 305 310 315 320  
 Glu Ala Ser Leu Ile Gly Arg Gly Ala Val Val Gly Pro Ala Pro Arg  
 325 330 335  
 Leu Pro Gln Ala His Arg Leu Val Ile Gly Asp His Ser Lys Val Tyr  
 340 345 350  
 Leu Thr Pro  
 355

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Thr Thr Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Arg Ser  
 1 5 10 15  
 Ala Tyr Val Arg Arg Leu Leu Ser Pro Gly Ala Pro Gly Gly Val Ala  
 20 25 30  
 Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Ser Leu Ala Arg Leu  
 35 40 45

His Ala Val Arg Asp His Pro Gly Leu Thr Phe Val Gln Gly Asp Val  
 50 55 60  
 Cys Asp Thr Ala Leu Val Asp Thr Leu Ala Ala Arg His Asp Asp Ile  
 65 70 75 80  
 Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Thr Asp Ser  
 85 90 95  
 Gly Ala Phe Thr Arg Thr Asn Val Leu Gly Thr Gln Val Leu Leu Asp  
 100 105 110  
 Ala Ala Leu Arg His Gly Val Arg Thr Phe Val His Val Ser Thr Asp  
 115 120 125  
 Glu Val Tyr Gly Ser Leu Pro His Gly Ala Ala Ala Glu Ser Asp Pro  
 130 135 140  
 Leu Leu Pro Thr Ser Pro Tyr Ala Ala Ser Lys Ala Ala Ser Asp Leu  
 145 150 155 160  
 Met Ala Leu Ala His His Arg Thr His Gly Leu Asp Val Arg Val Thr  
 165 170 175  
 Arg Cys Ser Asn Asn Phe Gly Pro His Gln His Pro Glu Lys Leu Ile  
 180 185 190  
 Pro Arg Phe Leu Thr Ser Leu Leu Ser Gly Gly Thr Val Pro Leu Tyr  
 195 200 205  
 Gly Asp Gly Arg His Val Arg Asp Trp Leu His Val Asp Asp His Val  
 210 215 220  
 Arg Ala Val Glu Leu Val Arg Val Ser Gly Arg Pro Gly Glu Ile Tyr  
 225 230 235 240  
 Asn Ile Gly Gly Gly Thr Ser Leu Pro Asn Leu Glu Leu Thr His Arg  
 245 250 255  
 Leu Leu Ala Leu Cys Gly Ala Gly Pro Glu Arg Ile Val His Val Glu  
 260 265 270  
 Asn Arg Lys Gly His Asp Arg Arg Tyr Ala Val Asp His Ser Lys Ile  
 275 280 285  
 Thr Ala Glu Leu Gly Tyr Arg Pro Arg Thr Asp Phe Ala Thr Ala Leu  
 290 295 300  
 Ala Asp Thr Ala Lys Trp Tyr Glu Arg His Glu Asp Trp Trp Arg Pro  
 305 310 315 320  
 Leu Leu Ala Ala Thr  
 325

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Met | Arg | Leu | Ala | Asp | Ile | Ala | Ala | Arg | Ala | Gly | Val | Ser | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Val | Ser | Arg | Val | Leu | Asn | Gly | Ala | Arg | Gly | Val | Ala | Thr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Arg | Asp | Ser | Val | Leu | Thr | Ala | Leu | Asp | Ala | Leu | Gly | Tyr | Glu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Arg | Gln | Arg | Arg | Ala | Glu | Leu | Val | Gly | Leu | Val | Thr | Pro | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Asn | Pro | Phe | Phe | Pro | Ala | Leu | Ala | Gln | Val | Met | Gly | Gln | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Thr | Arg | Gln | Gly | Tyr | Thr | Pro | Val | Leu | Ala | Thr | Gln | Thr | Pro | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Thr | Glu | Asp | Glu | Leu | Thr | Glu | Met | Leu | Val | Asp | Arg | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Ile | Ile | Phe | Val | Ser | Gly | Leu | His | Ala | Asp | Thr | Thr | Ala | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Gly | Arg | Tyr | Gly | Arg | Leu | His | Glu | Arg | Gln | Val | Pro | Phe | Val | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asn | Gly | Phe | Ser | Pro | Arg | Ile | Glu | Ala | Pro | Phe | Val | Ser | Pro | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Arg | Ala | Ala | Met | Arg | Leu | Ala | Val | Ala | His | Leu | Ala | Glu | Leu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Glu | Arg | Val | Gly | Leu | Ala | Val | Gly | Pro | Ala | Arg | Phe | Val | Pro | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Arg | Lys | Ile | Glu | Gly | Phe | Arg | Ala | Gly | Val | Arg | Glu | His | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ser | Ala | Arg | Glu | Ser | Glu | Glu | Leu | Val | Gln | His | Ser | Leu | Phe | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Glu | Gly | Gly | Gln | Ala | Ala | Ala | Ser | Ala | Leu | Ile | Asp | Leu | Gly | Cys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Ala | Val | Met | Cys | Ala | Ser | Asp | Met | Met | Ala | Leu | Gly | Ala | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala | Arg | Arg | Arg | Gly | Leu | Thr | Val | Pro | Gly | Asp | Ile | Ser | Val | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Phe | Asp | Asp | Ser | Pro | Leu | Met | Ala | Phe | Thr | Asp | Pro | Pro | Leu | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Ile | Arg | Gln | Pro | Val | Lys | Ala | Met | Gly | Gln | Val | Ala | Val | Asp | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Leu | Glu | Glu | Met | Ser | Gly | Thr | Pro | Pro | Pro | Arg | Thr | Glu | Phe | Val |
| 305 |     |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |

Phe Met Pro Glu Leu Val Val Arg Gly Ser Thr Ala Ala Gly Pro Arg  
325 330 335

Gly Gly Arg Arg Pro Ala His Gly Arg  
340 345

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Arg Gly Ile Ala Ala Thr Ala Leu Phe Ala Ala Val Ala Met  
1 5 10 15

Thr Ala Ser Ala Cys Gly Gly Gly Asp Asn Gly Gly Ser Gly Thr Asp  
20 25 30

Ala Gly Gly Thr Glu Leu Ser Gly Thr Val Thr Phe Trp Asp Thr Ser  
35 40 45

Asn Glu Ala Glu Lys Ala Thr Tyr Gln Ala Leu Ala Glu Gly Phe Glu  
50 55 60

Lys Glu His Pro Lys Val Asp Val Lys Tyr Val Asn Val Pro Phe Gly  
65 70 75 80

Glu Ala Asn Ala Lys Phe Lys Asn Ala Ala Gly Gly Asn Ser Gly Ala  
85 90 95

Pro Asp Val Met Arg Thr Glu Val Ala Trp Val Ala Asp Phe Ala Ser  
100 105 110

Ile Gly Tyr Leu Ala Pro Leu Asp Gly Thr Pro Ala Leu Asp Asp Gly  
115 120 125

Ser Asp His Leu Pro Gln Gly Gly Ser Thr Arg Tyr Glu Gly Lys Thr  
130 135 140

Tyr Ala Val Pro Gln Val Ile Asp Thr Leu Ala Leu Phe Tyr Asn Lys  
145 150 155 160

Glu Leu Leu Thr Lys Ala Gly Val Glu Val Pro Gly Ser Leu Ala Glu  
165 170 175

Leu Lys Thr Ala Ala Ala Glu Ile Thr Glu Lys Thr Gly Ala Ser Gly  
180 185 190

Leu Tyr Cys Gly Ala Thr Thr Arg Thr Trp Phe Leu Pro Tyr Leu Tyr  
195 200 205

Gly Glu Gly Gly Asp Leu Val Asp Glu Lys Asn Lys Thr Val Thr Val  
210 215 220

Asp Asp Glu Ala Gly Val Arg Ala Tyr Arg Val Ile Lys Asp Leu Val  
 225 230 235 240  
 Asp Ser Lys Ala Ala Ile Thr Asp Ala Ser Asp Gly Trp Asn Asn Met  
 245 250 255  
 Gln Asn Ala Phe Lys Ser Gly Lys Val Ala Met Met Val Asn Gly Pro  
 260 265 270  
 Trp Ala Ile Glu Asp Val Lys Ala Gly Ala Arg Phe Lys Asp Ala Gly  
 275 280 285  
 Asn Leu Gly Val Ala Pro Val Pro Ala Gly Ser Ala Gly Gln Gly Ser  
 290 295 300  
 Pro Gln Gly Gly Trp Asn Leu Ser Val Tyr Ala Gly Ser Lys Asn Leu  
 305 310 315 320  
 Asp Ala Ser Tyr Ala Phe Val Lys Tyr Met Ser Ser Ala Lys Val Gln  
 325 330 335  
 Gln Gln Thr Thr Glu Lys Leu Ser Leu Leu Pro Thr Arg Thr Ser Val  
 340 345 350  
 Tyr Glu Val Pro Ser Val Ala Asp Asn Glu Met Val Lys Phe Phe Lys  
 355 360 365  
 Pro Ala Val Asp Lys Ala Val Glu Arg Pro Trp Ile Ala Glu Gly Asn  
 370 375 380  
 Ala Leu Phe Glu Pro Ile Arg Leu Gln  
 385 390